



FRAV2002-0020 Sequence Listing.ST25.txt
SEQUENCE LISTING

<110> CORTI, Olga
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<120> METHOD FOR DETERMINING THE ABILITY OF A COMPOUND TO MODIFY THE INTERACTION BETWEEN PARKIN AND THE P38 PROTEIN

<130> FRAV2002-0020 US NP

<150> GB 0229934.5
<151> 2002-12-20

<150> US 60/396,929
<151> 2002-07-18

<160> 22

<170> PatentIn version 3.2

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<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(963)

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Met Pro Met Tyr Gln Val Lys Pro Tyr His Gly Gly Ala Pro Leu
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cgt gtg gag ctt ccc acc tgc atg tac cgg ctc ccc aac gtg cac ggc 96
Arg Val Glu Leu Pro Thr Cys Met Tyr Arg Leu Pro Asn Val His Gly
20 25 30

agg agc tac ggc cca gcg ccg ggc gct ggc cac gtg cag gaa gag tct 144
Arg Ser Tyr Gly Pro Ala Pro Gly Ala Gly His Val Gln Glu Glu Ser
35 40 45

aac ctg tct ctg caa gct ctt gag tcc cgc caa gat gat att tta aaa 192
Asn Leu Ser Leu Gln Ala Leu Glu Ser Arg Gln Asp Asp Ile Leu Lys
50 55 60

cgt ctg tat gag ttg aaa gct gca gtt gat ggc ctc tcc aag atg att 240
Arg Leu Tyr Glu Leu Lys Ala Ala Val Asp Gly Leu Ser Lys Met Ile
65 70 75 80

caa aca cca gat gca gac ttg gat gta acc aac ata atc caa gcg gat 288
Gln Thr Pro Asp Ala Asp Leu Asp Val Thr Asn Ile Ile Gln Ala Asp
85 90 95

gag ccc acg act tta acc acc aat gcg ctg gac ttg aat tca gtg ctt 336
Glu Pro Thr Thr Leu Thr Thr Asn Ala Leu Asp Leu Asn Ser Val Leu
100 105 110

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ggg aag gat tac ggg gcg ctg aaa gac atc gtg atc aac gca aac ccg Gly Lys Asp Tyr Gly Ala Leu Lys Asp Ile Val Ile Asn Ala Asn Pro 115 120 125	384
gcc tcc cct ccc ctc tcc ctg ctt gtg ctg cac agg ctg ctc tgt gag Ala Ser Pro Pro Leu Ser Leu Leu Val Leu His Arg Leu Leu Cys Glu 130 135 140	432
cac ttc agg gtc ctg tcc acg gtg cac acg cac tcc tcg gtc aag agc His Phe Arg Val Leu Ser Thr Val His Thr His Ser Ser Val Lys Ser 145 150 155 160	480
gtg cct gaa aac ctt ctc aag tgc ttt gga gaa cag aat aaa aaa cag Val Pro Glu Asn Leu Leu Lys Cys Phe Gly Glu Gln Asn Lys Lys Gln 165 170 175	528
ccc cgc caa gac tat cag ctg gga ttc act tta att tgg aag aat gtg Pro Arg Gln Asp Tyr Gln Leu Gly Phe Thr Leu Ile Trp Lys Asn Val 180 185 190	576
ccg aag acg cag atg aaa ttc agc atc cag acg atg tgc ccc atc gaa Pro Lys Thr Gln Met Lys Phe Ser Ile Gln Thr Met Cys Pro Ile Glu 195 200 205	624
ggc gaa ggg aac att gca cgt ttc ttg ttc tct ctg ttt ggc cag aag Gly Glu Gly Asn Ile Ala Arg Phe Leu Phe Ser Leu Phe Gly Gln Lys 210 215 220	672
cat aat gct gtc aac gca acc ctt ata gat agc tgg gta gat att gcg His Asn Ala Val Asn Ala Thr Leu Ile Asp Ser Trp Val Asp Ile Ala 225 230 235 240	720
att ttt cag tta aaa gag gga agc agt aaa gaa aaa gcc gct gtt ttc Ile Phe Gln Leu Lys Glu Gly Ser Ser Lys Glu Lys Ala Ala Val Phe 245 250 255	768
cgc tcc atg aac tct gct ctt ggg aag agc cct tgg ctc gct ggg aat Arg Ser Met Asn Ser Ala Leu Gly Lys Ser Pro Trp Leu Ala Gly Asn 260 265 270	816
gaa ctc acc gta gca gac gtg gtg ctg tgg tct gta ctc cag cag atc Glu Leu Thr Val Ala Asp Val Val Leu Trp Ser Val Leu Gln Gln Ile 275 280 285	864
gga ggc tgc agt gtg aca gtg cca gcc aat gtg cag agg tgg atg agg Gly Gly Cys Ser Val Thr Val Pro Ala Asn Val Gln Arg Trp Met Arg 290 295 300	912
tct tgt gaa aac ctg gct cct ttt aac acg gcc ctc aag ctc ctt aag Ser Cys Glu Asn Leu Ala Pro Phe Asn Thr Ala Leu Lys Leu Leu Lys 305 310 315 320	960
tga attgccgtaa ctgatttaa agggttttaga ttttaagaat ggtgctttt	1013
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tgtcaagtgt caataaaagc atcatgtaat taaaaaaaaaaa aaaaaaaaaa aactcgag	1131

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 <212> PRT
 <213> Homo sapiens

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Met Pro Met Tyr Gln Val Lys Pro Tyr His Gly Gly Gly Ala Pro Leu
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Arg Val Glu Leu Pro Thr Cys Met Tyr Arg Leu Pro Asn Val His Gly
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Arg Ser Tyr Gly Pro Ala Pro Gly Ala Gly His Val Gln Glu Glu Ser
35 40 45

Asn Leu Ser Leu Gln Ala Leu Glu Ser Arg Gln Asp Asp Ile Leu Lys
50 55 60

Arg Leu Tyr Glu Leu Lys Ala Ala Val Asp Gly Leu Ser Lys Met Ile
65 70 75 80

Gln Thr Pro Asp Ala Asp Leu Asp Val Thr Asn Ile Ile Gln Ala Asp
85 90 95

Glu Pro Thr Thr Leu Thr Thr Asn Ala Leu Asp Leu Asn Ser Val Leu
100 105 110

Gly Lys Asp Tyr Gly Ala Leu Lys Asp Ile Val Ile Asn Ala Asn Pro
115 120 125

Ala Ser Pro Pro Leu Ser Leu Leu Val Leu His Arg Leu Leu Cys Glu
130 135 140

His Phe Arg Val Leu Ser Thr Val His Thr His Ser Ser Val Lys Ser
145 150 155 160

Val Pro Glu Asn Leu Leu Lys Cys Phe Gly Glu Gln Asn Lys Lys Gln
165 170 175

Pro Arg Gln Asp Tyr Gln Leu Gly Phe Thr Leu Ile Trp Lys Asn Val
180 185 190

Pro Lys Thr Gln Met Lys Phe Ser Ile Gln Thr Met Cys Pro Ile Glu
195 200 205

Gly Glu Gly Asn Ile Ala Arg Phe Leu Phe Ser Leu Phe Gly Gln Lys
210 215 220

His Asn Ala Val Asn Ala Thr Leu Ile Asp Ser Trp Val Asp Ile Ala
225 230 235 240

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Ile Phe Gln Leu Lys Glu Gly Ser Ser Lys Glu Lys Ala Ala Val Phe
245 250 255

Arg Ser Met Asn Ser Ala Leu Gly Lys Ser Pro Trp Leu Ala Gly Asn
260 265 270

Glu Leu Thr Val Ala Asp Val Val Leu Trp Ser Val Leu Gln Gln Ile
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Gly Gly Cys Ser Val Thr Val Pro Ala Asn Val Gln Arg Trp Met Arg
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Ser Cys Glu Asn Leu Ala Pro Phe Asn Thr Ala Leu Lys Leu Leu Lys
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<212> PRT

<213> Homo sapiens

<400> 3

Met Pro Met Tyr Gln Val Lys Pro Tyr His Gly Gly Ala Pro Leu
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Arg Val Glu Leu Pro Thr Cys Met Tyr Arg Leu Pro Asn Val His Gly
20 25 30

Arg Ser Tyr Gly Pro Ala Pro Gly Ala Gly His Val Gln Glu Glu Ser
35 40 45

Asn Leu Ser Leu Gln Ala Leu Glu Ser Arg Gln Asp Asp Ile Leu Lys
50 55 60

Arg Leu Tyr Glu Leu Lys Ala Ala Val Asp Gly Leu Ser Lys Met Ile
65 70 75 80

Gln Thr Pro Asp Ala Asp Leu Asp Val Thr Asn Ile Ile Gln Ala Asp
85 90 95

Glu Pro Thr Thr Leu Thr Thr Asn Ala Leu Asp Leu Asn Ser Val Leu
100 105 110

Gly Lys Asp Tyr Gly Ala Leu Lys Asp Ile Val Ile Asn Ala Asn Pro
115 120 125

Ala Ser Pro Pro Leu Ser Leu Leu Val Leu His Arg Leu Leu Cys Glu
130 135 140

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His Phe Arg val Leu Ser Thr Val His Thr His Ser Ser Val Lys Ser
 145 150 155 160

Val Pro Glu Asn Leu Leu Lys Cys Phe Gly Glu Gln Asn Lys Lys Gln
 165 170 175

Pro Arg Gln Asp Tyr Gln Leu Gly Phe Thr Leu Ile Trp Lys Asn Val
 180 185 190

Pro Lys Thr Gln Met Lys Phe Ser Ile Gln Thr Met Cys Pro Ile Glu
 195 200 205

Gly Glu Gly Asn Ile Ala Arg Phe Leu Phe Ser Leu Phe Gly Gln Lys
 210 215 220

His Asn Ala Val Asn Ala Thr Leu Ile Asp Ser Trp Val Asp Ile Ala
 225 230 235 240

Ile Phe Gln Leu Lys Glu Gly Ser Ser Lys Glu Lys Ala Ala Val Phe
 245 250 255

Arg Ser Met Asn Ser Ala Leu Gly Lys Ser Pro Trp Leu Ala Gly Asn
 260 265 270

Glu Leu Thr Val Ala Asp Val Val Leu Trp Ser Val Leu Gln Gln Ile
 275 280 285

Gly Gly Cys Ser Val Thr Val Pro Ala Asn Val Gln Arg Trp Met Arg
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Ser Cys Glu Asn Leu Ala Pro Phe Asn Thr Ala Leu Lys Leu Leu Lys
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<211> 1233

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (78)..(1040)

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ttccttgggt tcccaacc atg ccg atg tac cag gta aag ccc tat cat gga 110
 Met Pro Met Tyr Gln Val Lys Pro Tyr His Gly
 1 5 10

ggc agc gca cct ctg cgt gta gag ctt cca acc tgc atg tac cgg ctc 158
 Gly Ser Ala Pro Leu Arg Val Glu Leu Pro Thr Cys Met Tyr Arg Leu

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15

20

25

ccc aac gtg cac agc aag acc acc agc ccc gcc acc gac gcg ggc cac	206
Pro Asn Val His Ser Lys Thr Thr Ser Pro Ala Thr Asp Ala Gly His	
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gtg cag gaa aca tcc gag cct tct ttg caa gcc ctt gaa tct cgc caa	254
Val Gln Glu Thr Ser Glu Pro Ser Leu Gln Ala Leu Glu Ser Arg Gln	
45 50 55	
gat gat att tta aaa cgc ttg tat gag ttg aag gca gca gtc gat ggc	302
Asp Asp Ile Leu Lys Arg Leu Tyr Glu Leu Lys Ala Ala Val Asp Gly	
60 65 70 75	
ctt tca aag atg att cac acc cca gat gca gac ttg gac gta acc aac	350
Leu Ser Lys Met Ile His Thr Pro Asp Ala Asp Leu Asp Val Thr Asn	
80 85 90	
atc ctg caa gct gat gag ccc aca act tta gcc aca aac aca ttg gac	398
Ile Leu Gln Ala Asp Glu Pro Thr Thr Leu Ala Thr Asn Thr Leu Asp	
95 100 105	
ttg aat tcc gtg ctt gga aag gac tat ggg gcg ctg aaa gac att gtg	446
Leu Asn Ser Val Leu Gly Lys Asp Tyr Gly Ala Leu Lys Asp Ile Val	
110 115 120	
atc aac gca aac cca gcc tcc cca cca ctg tcc ctg ctt gtg ctg cac	494
Ile Asn Ala Asn Pro Ala Ser Pro Pro Leu Ser Leu Leu Val Leu His	
125 130 135	
agg ctg ctc tgt gaa cgc tac agg gtc ctg tcc act gtg cac aca cat	542
Arg Leu Leu Cys Glu Arg Tyr Arg Val Leu Ser Thr Val His Thr His	
140 145 150 155	
tcg tct gtc aag aat gtg ccc gag aat ctt gtc aag tgc ttc ggg gag	590
Ser Ser Val Lys Asn Val Pro Glu Asn Leu Val Lys Cys Phe Gly Glu	
160 165 170	
cag gct agg aag cag tcc cgc cac gag tat cag ctg ggc ttc act ctg	638
Gln Ala Arg Lys Gln Ser Arg His Glu Tyr Gln Leu Gly Phe Thr Leu	
175 180 185	
att tgg aag aat gtg ccc aag aca cag atg aag ttc agt gta caa acc	686
Ile Trp Lys Asn Val Pro Lys Thr Gln Met Lys Phe Ser Val Gln Thr	
190 195 200	
atg tgc ccc att gaa gga gaa ggg aac atc gca cgt ttc ctg ttc tct	734
Met Cys Pro Ile Glu Gly Glu Gly Asn Ile Ala Arg Phe Leu Phe Ser	
205 210 215	
ctg ttt ggc cag aag cat aat gct gtc acc ctc acc ctc atc gat agc	782
Leu Phe Gly Gln Lys His Asn Ala Val Thr Leu Thr Leu Ile Asp Ser	
220 225 230 235	
tgg gtg gat atc gcc atg ttt cag ctt cga gaa ggc agc agt aaa gaa	830
Trp Val Asp Ile Ala Met Phe Gln Leu Arg Glu Gly Ser Ser Lys Glu	
240 245 250	
aaa gcg gcc gtg ttc cgc tct atg aac tcc gct ttg ggg agg agc ccg	878
Lys Ala Ala Val Phe Arg Ser Met Asn Ser Ala Leu Gly Arg Ser Pro	
255 260 265	
tgg ctg gtt gga aat gag ctc act gtg gca gat gtg gtg ctg tgg tct	926

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Trp	Leu	Val	Gly	Asn	Glu	Leu	Thr	Val	Ala	Asp	Val	Val	Leu	Trp	Ser
270					275								280		
gtg	ctc	cag	cag	act	ggg	ggc	agc	agt	ggg	gca	gca	ccc	acc	aat	gtg
Val	Leu	Gln	Gln	Thr	Gly	Gly	Ser	Ser	Gly	Ala	Ala	Pro	Thr	Asn	Val
285				290					295						
cag	cg	tgg	ctt	aag	tcc	tgt	gaa	aac	ctg	gcc	ccc	ttc	agc	act	gcc
Gln	Arg	Trp	Leu	Lys	Ser	Cys	Glu	Asn	Leu	Ala	Pro	Phe	Ser	Thr	Ala
300				305					310					315	
ctt	cag	ctc	ctt	aag	tga	attcgagcag	cttgttgc	agggttcaac							1070
Leu	Gln	Leu	Leu	Lys											
				320											
agaagaatgg	tacggcttcc	agtctgttgt	cagaaaggga	cttgtccaat	aaagtaccat										1130
atcatctaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa										1190
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaa										1233

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<213> Mus musculus
<400> 5

Met Pro Met Tyr Gln Val Lys Pro Tyr His Gly Gly Ser Ala Pro Leu
1 5 10 15

Arg Val Glu Leu Pro Thr Cys Met Tyr Arg Leu Pro Asn Val His Ser
20 25 30

Lys Thr Thr Ser Pro Ala Thr Asp Ala Gly His Val Gln Glu Thr Ser
35 40 45

Glu Pro Ser Leu Gln Ala Leu Glu Ser Arg Gln Asp Asp Ile Leu Lys
50 55 60

Arg Leu Tyr Glu Leu Lys Ala Ala Val Asp Gly Leu Ser Lys Met Ile
65 70 75 80

His Thr Pro Asp Ala Asp Leu Asp Val Thr Asn Ile Leu Gln Ala Asp
85 90 95

Glu Pro Thr Thr Leu Ala Thr Asn Thr Leu Asp Leu Asn Ser Val Leu
100 105 110

Gly Lys Asp Tyr Gly Ala Leu Lys Asp Ile Val Ile Asn Ala Asn Pro
115 120 125

Ala Ser Pro Pro Leu Ser Leu Leu Val Leu His Arg Leu Leu Cys Glu
130 135 140

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Arg Tyr Arg Val Leu Ser Thr Val His Thr His Ser Ser Val Lys Asn
145 150 155 160

Val Pro Glu Asn Leu Val Lys Cys Phe Gly Glu Gln Ala Arg Lys Gln
165 170 175

Ser Arg His Glu Tyr Gln Leu Gly Phe Thr Leu Ile Trp Lys Asn Val
180 185 190

Pro Lys Thr Gln Met Lys Phe Ser Val Gln Thr Met Cys Pro Ile Glu
195 200 205

Gly Glu Gly Asn Ile Ala Arg Phe Leu Phe Ser Leu Phe Gly Gln Lys
210 215 220

His Asn Ala Val Thr Leu Thr Leu Ile Asp Ser Trp Val Asp Ile Ala
225 230 235 240

Met Phe Gln Leu Arg Glu Gly Ser Ser Lys Glu Lys Ala Ala Val Phe
245 250 255

Arg Ser Met Asn Ser Ala Leu Gly Arg Ser Pro Trp Leu Val Gly Asn
260 265 270

Glu Leu Thr Val Ala Asp Val Val Leu Trp Ser Val Leu Gln Gln Thr
275 280 285

Gly Gly Ser Ser Gly Ala Ala Pro Thr Asn Val Gln Arg Trp Leu Lys
290 295 300

Ser Cys Glu Asn Leu Ala Pro Phe Ser Thr Ala Leu Gln Leu Leu Lys
305 310 315 320

<210> 6
<211> 320

<212> PRT
<213> Mus musculus

<400> 6

Met Pro Met Tyr Gln Val Lys Pro Tyr His Gly Gly Ser Ala Pro Leu
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Arg Val Glu Leu Pro Thr Cys Met Tyr Arg Leu Pro Asn Val His Ser
20 25 30

Lys Thr Thr Ser Pro Ala Thr Asp Ala Gly His Val Gln Glu Thr Ser
35 40 45

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Glu Pro Ser Leu Gln Ala Leu Glu Ser Arg Gln Asp Asp Ile Leu Lys
50 55 60

Arg Leu Tyr Glu Leu Lys Ala Ala Val Asp Gly Leu Ser Lys Met Ile
65 70 75 80

His Thr Pro Asp Ala Asp Leu Asp Val Thr Asn Ile Leu Gln Ala Asp
85 90 95

Glu Pro Thr Thr Leu Ala Thr Asn Thr Leu Asp Leu Asn Ser Val Leu
100 105 110

Gly Lys Asp Tyr Gly Ala Leu Lys Asp Ile Val Ile Asn Ala Asn Pro
115 120 125

Ala Ser Pro Pro Leu Ser Leu Leu Val Leu His Arg Leu Leu Cys Glu
130 135 140

Arg Tyr Arg Val Leu Ser Thr Val His Thr His Ser Ser Val Lys Asn
145 150 155 160

Val Pro Glu Asn Leu Val Lys Cys Phe Gly Glu Gln Ala Arg Lys Gln
165 170 175

Ser Arg His Glu Tyr Gln Leu Gly Phe Thr Leu Ile Trp Lys Asn Val
180 185 190

Pro Lys Thr Gln Met Lys Phe Ser Val Gln Thr Met Cys Pro Ile Glu
195 200 205

Gly Glu Gly Asn Ile Ala Arg Phe Leu Phe Ser Leu Phe Gly Gln Lys
210 215 220

His Asn Ala Val Thr Leu Thr Leu Ile Asp Ser Trp Val Asp Ile Ala
225 230 235 240

Met Phe Gln Leu Arg Glu Gly Ser Ser Lys Glu Lys Ala Ala Val Phe
245 250 255

Arg Ser Met Asn Ser Ala Leu Gly Arg Ser Pro Trp Leu Val Gly Asn
260 265 270

Glu Leu Thr Val Ala Asp Val Val Leu Trp Ser Val Leu Gln Gln Thr
275 280 285

Gly Gly Ser Ser Gly Ala Ala Pro Thr Asn Val Gln Arg Trp Leu Lys

Ser Cys Glu Asn Leu Ala Pro Phe Ser Thr Ala Leu Gln Leu Leu Lys
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 Met Ile Val Phe Val
 1 5
 agg ttc aac tcc agc cat ggt ttc cca gtg gag gtc gat tct gac acc 164
 Arg Phe Asn Ser Ser His Gly Phe Pro Val Glu Val Asp Ser Asp Thr
 10 15 20
 agc atc ttc cag ctc aag gag gtg gtt gct aag cga cag ggg gtt ccg 212
 Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys Arg Gln Gly Val Pro
 25 30 35
 gct gac cag ttg cgt gtg att ttc gca ggg aag gag ctg agg aat gac 260
 Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys Glu Leu Arg Asn Asp
 40 45 50
 tgg act gtg cag aat tgt gac ctg gat cag cag agc att gtt cac att 308
 Trp Thr Val Gln Asn Cys Asp Leu Asp Gln Gln Ser Ile Val His Ile
 55 60 65
 gtg cag aga ccg tgg aga aaa ggt caa gaa atg aat gca act gga ggc 356
 Val Gln Arg Pro Trp Arg Lys Gly Gln Glu Met Asn Ala Thr Gly Gly
 70 75 80 85
 gac gac ccc aga aac gcg gcg gga ggc tgt gag cgg gag ccc cag agc 404
 Asp Asp Pro Arg Asn Ala Ala Gly Gly Cys Glu Arg Glu Pro Gln Ser
 90 95 100
 ttg act cggtt gac ctc agc agc tca gtc ctc cca gga gac tct gtg 452
 Leu Thr Arg Val Asp Leu Ser Ser Val Leu Pro Gly Asp Ser Val
 105 110 115
 ggg ctg gct gtc att ctg cac act gac agc agg aag gac tca cca cca 500
 Gly Leu Ala Val Ile Leu His Thr Asp Ser Arg Lys Asp Ser Pro Pro
 120 125 130
 gct gga agt cca gca ggt aga tca atc tac aac agc ttt tat gtg tat 548
 Ala Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn Ser Phe Tyr Val Tyr
 135 140 145
 tgc aaa ggc ccc tgt caa aga gtg cag ccg gga aaa ctc agg gta cag 596
 Cys Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln
 150 155 160 165

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170								175						180		
tgc	tgg	gat	gat	gtt	tta	att	cca	aac	cgg	atg	agt	ggt	gaa	tgc	caa	692
Cys	Trp	Asp	Asp	Val	Leu	Ile	Pro	Asn	Arg	Met	Ser	Gly	Glu	Cys	Gln	
185							190						195			
tcc	cca	cac	tgc	cct	ggg	act	agt	gca	gaa	ttt	ttc	ttt	aaa	tgt	gga	740
Ser	Pro	His	Cys	Pro	Gly	Thr	Ser	Ala	Glu	Phe	Phe	Phe	Lys	Cys	Gly	
200							205						210			
gca	cac	ccc	acc	tct	gac	aag	gaa	aca	cca	gta	gct	ttg	cac	ctg	atc	788
Ala	His	Pro	Thr	Ser	Asp	Lys	Glu	Thr	Pro	Val	Ala	Leu	His	Leu	Ile	
215						220					225					
gca	aca	aat	agt	cgg	aac	atc	act	tgc	att	acg	tgc	aca	gac	gtc	agg	836
Ala	Thr	Asn	Ser	Arg	Asn	Ile	Thr	Cys	Ile	Thr	Cys	Thr	Asp	Val	Arg	
230						235				240				245		
agc	ccc	gtc	ctg	gtt	ttc	cag	tgc	aac	tcc	cgc	cac	gtg	att	tgc	tta	884
Ser	Pro	Val	Leu	Val	Phe	Gln	Cys	Asn	Ser	Arg	His	Val	Ile	Cys	Leu	
250						255					260					
gac	tgt	ttc	cac	tta	tac	tgt	gtg	aca	aga	ctc	aat	gat	cgg	cag	ttt	932
Asp	Cys	Phe	His	Leu	Tyr	Cys	Val	Thr	Arg	Leu	Asn	Asp	Arg	Gln	Phe	
265						270					275					
gtt	cac	gac	cct	caa	ctt	ggc	tac	tcc	ctg	cct	tgt	gtg	gct	ggc	tgt	980
Val	His	Asp	Pro	Gln	Leu	Gly	Tyr	Ser	Leu	Pro	Cys	Val	Ala	Gly	Cys	
280						285					290					
ccc	aac	tcc	ttg	att	aaa	gag	ctc	cat	cac	ttc	agg	att	ctg	gga	gaa	1028
Pro	Asn	Ser	Leu	Ile	Lys	Glu	Leu	His	His	Phe	Arg	Ile	Leu	Gly	Glu	
295						300					305					
gag	cag	tac	aac	cgg	tac	cag	cag	tat	ggt	gca	gag	gag	tgt	gtc	ctg	1076
Glu	Gln	Tyr	Asn	Arg	Tyr	Gln	Gln	Tyr	Gly	Ala	Glu	Glu	Cys	Val	Leu	
310						315				320				325		
cag	atg	ggg	ggc	gtg	tta	tgc	ccc	cgc	cct	ggc	tgt	gga	gcg	ggg	ctg	1124
Gln	Met	Gly	Gly	Val	Leu	Cys	Pro	Arg	Pro	Gly	Cys	Gly	Ala	Gly	Leu	
330						335					340					
ctg	ccg	gag	cct	gac	cag	agg	aaa	gtc	acc	tgc	gaa	ggg	ggc	aat	goc	1172
Leu	Pro	Glu	Pro	Asp	Gln	Arg	Lys	Val	Thr	Cys	Glu	Gly	Gly	Asn	Gly	
345						350					355					
ctg	ggc	tgt	ggg	ttt	gcc	ttc	tgc	cgg	gaa	tgt	aaa	gaa	gcg	tac	cat	1220
Leu	Gly	Cys	Gly	Phe	Ala	Phe	Cys	Arg	Glu	Cys	Lys	Glu	Ala	Tyr	His	
360						365					370					
gaa	ggg	gag	tgc	agt	gcc	gta	ttt	gaa	gcc	tca	gga	aca	act	act	cag	1268
Glu	Gly	Glu	Cys	Ser	Ala	Val	Phe	Glu	Ala	Ser	Gly	Thr	Thr	Thr	Gln	
375						380					385					
gcc	tac	aga	gtc	gat	gaa	aga	gcc	gcc	gag	cag	gct	cgt	tgg	gaa	gca	1316
Ala	Tyr	Arg	Val	Asp	Glu	Arg	Ala	Ala	Glu	Gln	Ala	Arg	Trp	Glu	Ala	
390						395					400			405		
gcc	tcc	aaa	gaa	acc	atc	aag	aaa	acc	acc	aag	ccc	tgt	ccc	cgc	tgc	1364
Ala	Ser	Lys	Glu	Thr	Ile	Lys	Lys	Thr	Thr	Lys	Pro	Cys	Pro	Arg	Cys	

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410

415

420

cat gta cca gtg gaa aaa aat gga ggc tgc atg cac atg aag tgt ccg	1412
His Val Pro Val Glu Lys Asn Gly Gly Cys Met His Met Lys Cys Pro	
425 430 435	
cag ccc cag tgc agg ctc gag tgg tgc tgg aac tgt ggc tgc gag tgg	1460
Gln Pro Gln Cys Arg Leu Glu Trp Cys Trp Asn Cys Gly Cys Glu Trp	
440 445 450	
aac cgc gtc tgc atg ggg gac cac tgg ttc gac gtg tag ccagggcggc	1509
Asn Arg Val Cys Met Gly Asp His Trp Phe Asp Val	
455 460 465	
cgggcgcccc atcgccacat cctggggag cataccagt gtctaccttc attttctaatt	1569
tctctttca aacacacaca cacacgcgcg cgcgcgaca cacactcttc aagtttttt	1629
caaagtccaa ctacagccaa attgcagaag aaactcctgg atccctttca ctatgtccat	1689
aaaaaacagc agagtaaaat tacagaagaa gctcctgaat cccttcagt ttgtccacac	1749
aagacagcag agccatctgc gacaccacca acaggcggtc tcagcctccg gatgacacaa	1809
ataccagagc acagattcaa gtgcaatcca tgtatctgta tgggtcattc tcacctgaat	1869
tcgagacagg cagaatcagt agctggagag agagttctca catttaatat cctgccttt	1929
accttcagta aacaccatga agatgccatt gacaagggtgt ttctctgtaa aatgaactgc	1989
agtgggtct ccaaactaga ttcatggctt taacagtaat gttcttattt aaattttcag	2049
aaagcatcta ttcccaaaga accccaggca atagtcaaaa acatttgtt atccttaaga	2109
attccatcta tataaatcgc attaatcgaa ataccaacta tgtgtaaatc aacttgcac	2169
aaagtgagaa attatgaaag ttaattgaa tggtaatgt ttgaattaca gggaaagaaat	2229
caagttaatg tactttcatt cccttcattg atttgcact ttagaaagaa attgttttc	2289
tgaaagtatc accaaaaaat ctatagtttgcatttgc aacttggaga	2349
ttttgctaat acatttggct ccactgtaaa ttatagat aaagtgccta taaaggaaac	2409
acgtttagaa atgatttcaa aatgatattc aatcttaaca aaagtgaaca ttattaaatc	2469
agaatctta aagaggagcc ttccagaac taccaaaatg aagacacgccc cgactctc	2529
catcagaagg gtttataccc ctttggcaca ccctctgtt ccaatctgca agtcccagg	2589
agctctgcat accaggggtt cccaggaga gaccttctct taggacagta aactcactag	2649
aatattcctt atggtgacat ggattggatt tcagttcaat caaactttca gcttttttt	2709
cagccattca caacacaatc aaaagattaa caacactgca tgcggcaaac cgcatgctct	2769
tacccacact acgcagaaga gaaagtacaa ccactatctt ttgttctacc tgtattgtct	2829
gacttctcag gaagatcgtg aacataactg agggcatgag tctcactagc acatggaggc	2889
cctttggat ttagagactg taaattatta aatcgcaac agggcttctc ttttagatg	2949
tagcactgaa a	2960

FRAV2002-0020 Sequence Listing.ST25.txt

<210> 8
<211> 465
<212> PRT
<213> Homo sapiens

<400> 8

Met Ile Val Phe Val Arg Phe Asn Ser Ser His Gly Phe Pro Val Glu
1 5 10 15

Val Asp Ser Asp Thr Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys
20 25 30

Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys
35 40 45

Glu Leu Arg Asn Asp Trp Thr Val Gln Asn Cys Asp Leu Asp Gln Gln
50 55 60

Ser Ile Val His Ile Val Gln Arg Pro Trp Arg Lys Gly Gln Glu Met
65 70 75 80

Asn Ala Thr Gly Gly Asp Asp Pro Arg Asn Ala Ala Gly Gly Cys Glu
85 90 95

Arg Glu Pro Gln Ser Leu Thr Arg Val Asp Leu Ser Ser Val Leu
100 105 110

Pro Gly Asp Ser Val Gly Leu Ala Val Ile Leu His Thr Asp Ser Arg
115 120 125

Lys Asp Ser Pro Pro Ala Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn
130 135 140

Ser Phe Tyr Val Tyr Cys Lys Gly Pro Cys Gln Arg Val Gln Pro Gly
145 150 155 160

Lys Leu Arg Val Gln Cys Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu
165 170 175

Thr Gln Gly Pro Ser Cys Trp Asp Asp Val Leu Ile Pro Asn Arg Met
180 185 190

Ser Gly Glu Cys Gln Ser Pro His Cys Pro Gly Thr Ser Ala Glu Phe
195 200 205

Phe Phe Lys Cys Gly Ala His Pro Thr Ser Asp Lys Glu Thr Pro Val
210 215 220

FRAV2002-0020 Sequence Listing.ST25.txt

Ala Leu His Leu Ile Ala Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr
225 230 235 240

Cys Thr Asp Val Arg Ser Pro Val Leu Val Phe Gln Cys Asn Ser Arg
245 250 255

His Val Ile Cys Leu Asp Cys Phe His Leu Tyr Cys Val Thr Arg Leu
260 265 270

Asn Asp Arg Gln Phe Val His Asp Pro Gln Leu Gly Tyr Ser Leu Pro
275 280 285

Cys Val Ala Gly Cys Pro Asn Ser Leu Ile Lys Glu Leu His His Phe
290 295 300

Arg Ile Leu Gly Glu Glu Gln Tyr Asn Arg Tyr Gln Gln Tyr Gly Ala
305 310 315 320

Glu Glu Cys Val Leu Gln Met Gly Gly Val Leu Cys Pro Arg Pro Gly
325 330 335

Cys Gly Ala Gly Leu Leu Pro Glu Pro Asp Gln Arg Lys Val Thr Cys
340 345 350

Glu Gly Gly Asn Gly Leu Gly Cys Gly Phe Ala Phe Cys Arg Glu Cys
355 360 365

Lys Glu Ala Tyr His Glu Gly Glu Cys Ser Ala Val Phe Glu Ala Ser
370 375 380

Gly Thr Thr Thr Gln Ala Tyr Arg Val Asp Glu Arg Ala Ala Glu Gln
385 390 395 400

Ala Arg Trp Glu Ala Ala Ser Lys Glu Thr Ile Lys Lys Thr Thr Lys
405 410 415

Pro Cys Pro Arg Cys His Val Pro Val Glu Lys Asn Gly Gly Cys Met
420 425 430

His Met Lys Cys Pro Gln Pro Gln Cys Arg Leu Glu Trp Cys Trp Asn
435 440 445

Cys Gly Cys Glu Trp Asn Arg Val Cys Met Gly Asp His Trp Phe Asp
450 455 460

val

465

<210> 9
<211> 465
<212> PRT
<213> Homo sapiens

<400> 9

Met Ile Val Phe Val Arg Phe Asn Ser Ser His Gly Phe Pro Val Glu
1 5 10 15

Val Asp Ser Asp Thr Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys
20 25 30

Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys
35 40 45

Glu Leu Arg Asn Asp Trp Thr Val Gln Asn Cys Asp Leu Asp Gln Gln
50 55 60

Ser Ile Val His Ile Val Gln Arg Pro Trp Arg Lys Gly Gln Glu Met
65 70 75 80

Asn Ala Thr Gly Gly Asp Asp Pro Arg Asn Ala Ala Gly Gly Cys Glu
85 90 95

Arg Glu Pro Gln Ser Leu Thr Arg Val Asp Leu Ser Ser Ser Val Leu
100 105 110

Pro Gly Asp Ser Val Gly Leu Ala Val Ile Leu His Thr Asp Ser Arg
115 120 125

Lys Asp Ser Pro Pro Ala Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn
130 135 140

Ser Phe Tyr Val Tyr Cys Lys Gly Pro Cys Gln Arg Val Gln Pro Gly
145 150 155 160

Lys Leu Arg Val Gln Cys Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu
165 170 175

Thr Gln Gly Pro Ser Cys Trp Asp Asp Val Leu Ile Pro Asn Arg Met
180 185 190

Ser Gly Glu Cys Gln Ser Pro His Cys Pro Gly Thr Ser Ala Glu Phe
195 200 205

Phe Phe Lys Cys Gly Ala His Pro Thr Ser Asp Lys Glu Thr Pro Val
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210

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215 220

Ala Leu His Leu Ile Ala Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr
225 230 235 240

Cys Thr Asp Val Arg Ser Pro Val Leu Val Phe Gln Cys Asn Ser Arg
245 250 255

His Val Ile Cys Leu Asp Cys Phe His Leu Tyr Cys Val Thr Arg Leu
260 265 270

Asn Asp Arg Gln Phe Val His Asp Pro Gln Leu Gly Tyr Ser Leu Pro
275 280 285

Cys Val Ala Gly Cys Pro Asn Ser Leu Ile Lys Glu Leu His His Phe
290 295 300

Arg Ile Leu Gly Glu Glu Gln Tyr Asn Arg Tyr Gln Gln Tyr Gly Ala
305 310 315 320

Glu Glu Cys Val Leu Gln Met Gly Gly Val Leu Cys Pro Arg Pro Gly
325 330 335

Cys Gly Ala Gly Leu Leu Pro Glu Pro Asp Gln Arg Lys Val Thr Cys
340 345 350

Glu Gly Gly Asn Gly Leu Gly Cys Gly Phe Ala Phe Cys Arg Glu Cys
355 360 365

Lys Glu Ala Tyr His Glu Gly Glu Cys Ser Ala Val Phe Glu Ala Ser
370 375 380

Gly Thr Thr Thr Gln Ala Tyr Arg Val Asp Glu Arg Ala Ala Glu Gln
385 390 395 400

Ala Arg Trp Glu Ala Ala Ser Lys Glu Thr Ile Lys Lys Thr Thr Lys
405 410 415

Pro Cys Pro Arg Cys His Val Pro Val Glu Lys Asn Gly Gly Cys Met
420 425 430

His Met Lys Cys Pro Gln Pro Gln Cys Arg Leu Glu Trp Cys Trp Asn
435 440 445

Cys Gly Cys Glu Trp Asn Arg Val Cys Met Gly Asp His Trp Phe Asp
450 455 460

FRAV2002-0020 Sequence Listing.ST25.txt

val
465

<210> 10
<211> 471
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (1)..(471)

<400> 10
gga agt cca gca ggt aga tca atc tac aac agc ttt tat gtg tat tgc 48
Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn Ser Phe Tyr Val Tyr Cys
1 5 10 15

aaa ggc ccc tgt caa aga gtg cag ccg gga aaa ctc agg gta cag tgc 96
 Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln Cys
 20 25 30

agc acc tgc agg cag gca acg ctc acc ttg acc cag ggt cca tct tgc 144
 Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu Thr Gln Gly Pro Ser Cys
 35 40 45

tgg gat gat gtt tta att cca aac cgg atg agt ggt gaa tgc caa tcc	192
Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser	
50 55 60	

cca cac tgc cct ggg act agt gca gaa ttt ttc ttt aaa tgt gga gca 240
 Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly Ala
 65 70 75 80

cac ccc acc tct gac aag gaa aca tca gta gct ttg cac ctg atc gca 288
 His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile Ala
 85 90 95

aca aat agt cg^g aac atc act tgc att acg tgc aca gac gtc agg agc 336
 Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg Ser
 100 105 110

ccc gtc ctg gtt ttc cag tgc aac tcc cgc cac gtg att tgc tta gac 384
 Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu Asp
 115 120 125

tgt ttc cac tta tac tgt gtg aca aga ctc aat gat cg_g cag ttt gtt 432
 Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val
 130 135 140

cac gac cct caa ctt ggc tac tcc ctg cct tgt gtg tag
 His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val
 145 150 155 471

<210> 11
<211> 156
<212> PRT
<213> *Homo sapiens*

<400> 11

FRAV2002-0020 Sequence Listing.ST25.txt

Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn Ser Phe Tyr Val Tyr Cys
1 5 10 15

Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln Cys
20 25 30

Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu Thr Gln Gly Pro Ser Cys
35 40 45

Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser
50 55 60

Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly Ala
65 70 75 80

His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile Ala
85 90 95

Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg Ser
100 105 110

Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu Asp
115 120 125

Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val
130 135 140

His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val
145 150 155

<210> 12

<211> 156

<212> PRT

<213> Homo sapiens

<400> 12

Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn Ser Phe Tyr Val Tyr Cys
1 5 10 15

Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln Cys
20 25 30

Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu Thr Gln Gly Pro Ser Cys
35 40 45

Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser
50 55 60

FRAV2002-0020 Sequence Listing.ST25.txt

Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly Ala
 65 70 75 80

His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile Ala
 85 90 95

Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg Ser
 100 105 110

Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu Asp
 115 120 125

Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val
 130 135 140

His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val
 145 150 155

<210> 13
 <211> 1470
 <212> DNA
 <213> Rattus norvegicus

<220>
 <221> CDS
 <222> (1)..(1470)

<400> 13	48
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Met Ile Val Phe Val Arg Phe Asn Ser Ser Tyr Gly Phe Pro Val Glu	
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gtc gat tct gac acc agc atc ttc cag ctc aag gaa gtg gtt gct aag	96
Val Asp Ser Asp Thr Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys	
20 25 30	
cga cag ggg gtt cca gct gac cag ctg cga gtg att ttt gct ggg aag	144
Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys	
35 40 45	
gag ctg cag aat cac ctg aca gta cag cat ccc cag gat ggt ttc tgt	192
Glu Leu Gln Asn His Leu Thr Val Gln His Pro Gln Asp Gly Phe Cys	
50 55 60	
cat aag tct cac ctt gct gtt cat aat ctc tct cag cag gac gtc aca	240
His Lys Ser His Leu Ala Val His Asn Leu Ser Gln Gln Asp Val Thr	
65 70 75 80	
cag aac tgt gac ctg gaa caa cag agt atc gtt cac ata gta cag aga	288
Gln Asn Cys Asp Leu Glu Gln Gln Ser Ile Val His Ile Val Gln Arg	
85 90 95	
cca cag agg aaa agt cac gaa aca aat gcc tct gga ggg gac aaa ccc	336
Pro Gln Arg Lys Ser His Glu Thr Asn Ala Ser Gly Gly Asp Lys Pro	
100 105 110	

FRAV2002-0020 Sequence Listing.ST25.txt

cag	agc	acc	ccg	gag	ggc	tcc	ata	tgg	gag	ccc	aga	agc	ttg	act	cga		384
Gln	Ser	Thr	Pro	Glu	Gly	Ser	Ile	Trp	Glu	Pro	Arg	Ser	Leu	Thr	Arg		
115				120					125								
gtg	gac	ctc	agc	agc	cat	atc	ctg	cca	gcg	gac	tcc	gtg	ggg	ctg	gca		432
Val	Asp	Leu	Ser	Ser	His	Ile	Leu	Pro	Ala	Asp	Ser	Val	Gly	Leu	Ala		
130				135					140								
gtc	att	ctg	gac	aca	gac	agc	aag	agt	gac	tca	gaa	gca	gcc	aga	ggt		480
Val	Ile	Leu	Asp	Thr	Asp	Ser	Lys	Ser	Asp	Ser	Glu	Ala	Ala	Arg	Gly		
145				150					155						160		
cca	gaa	gct	aaa	ccc	acc	tac	cac	agc	ttt	ttt	gtc	tac	tgc	aaa	ggc		528
Pro	Glu	Ala	Lys	Pro	Thr	Tyr	His	Ser	Phe	Phe	Val	Tyr	Cys	Lys	Gly		
				165					170						175		
ccc	tgc	cac	aag	gtc	cag	cct	ggg	aaa	ctc	cga	gtt	cag	tgc	ggc	acc		576
Pro	Cys	His	Lys	Val	Gln	Pro	Gly	Lys	Leu	Arg	Val	Gln	Cys	Gly	Thr		
				180					185						190		
tgc	aga	caa	gca	acc	ctc	acc	ttg	gcc	cag	ggc	cca	tct	tgc	tgg	gat		624
Cys	Arg	Gln	Ala	Thr	Leu	Thr	Leu	Ala	Gln	Gly	Pro	Ser	Cys	Trp	Asp		
				195					200						205		
gat	gtc	tta	att	cca	aac	cgg	atg	agt	gga	gag	tgt	caa	tct	cca	gac		672
Asp	Val	Leu	Ile	Pro	Asn	Arg	Met	Ser	Gly	Glu	Cys	Gln	Ser	Pro	Asp		
				210					215						220		
tgc	cct	ggg	aca	aga	gct	gaa	ttt	ttc	ttt	aaa	tgt	gga	gca	cac	cca		720
Cys	Pro	Gly	Thr	Arg	Ala	Glu	Phe	Phe	Phe	Lys	Cys	Gly	Ala	His	Pro		
				225					230						240		
acc	tca	gac	aag	gac	aca	tca	gta	gct	ttg	aac	ctg	atc	acc	aac	aac		768
Thr	Ser	Asp	Lys	Asp	Thr	Ser	Val	Ala	Leu	Asn	Leu	Ile	Thr	Asn	Asn		
				245					250						255		
agc	cgc	agc	atc	ccc	tgc	atc	gcg	tgc	acg	gat	gtc	agg	aac	cct	gtc		816
Ser	Arg	Ser	Ile	Pro	Cys	Ile	Ala	Cys	Thr	Asp	Val	Arg	Asn	Pro	Val		
				260					265						270		
ttg	gtc	ttc	caa	tgt	aac	cac	cgc	cac	gtg	atc	tgt	ttg	gac	tgc	ttc		864
Leu	Val	Phe	Gln	Cys	Asn	His	Arg	His	Val	Ile	Cys	Leu	Asp	Cys	Phe		
				275					280						285		
cac	ttg	tac	tgt	gtc	aca	agg	ctc	aac	gat	cg	cag	ttt	gtc	cac	gac		912
His	Leu	Tyr	Cys	Val	Thr	Arg	Leu	Asn	Asp	Arg	Gln	Phe	Val	His	Asp		
				290					295						300		
gct	cag	ctt	ggc	tac	tcg	ctg	ccg	tgt	gtg	gct	ggc	tgt	ccc	aac	tcc		960
Ala	Gln	Leu	Gly	Tyr	Ser	Leu	Pro	Cys	Val	Ala	Gly	Cys	Pro	Asn	Ser		
				305					310						315		
ctg	att	aaa	gag	ctc	cat	cac	ttc	agg	atc	ctt	gga	gaa	gag	cag	tac		1008
Leu	Ile	Lys	Glu	Leu	His	His	Phe	Arg	Ile	Leu	Gly	Glu	Glu	Gln	Tyr		
				325					330						335		
aac	agg	tac	cag	cag	tat	ggt	gcc	gag	gag	tgc	gtg	ctg	cag	atg	gga		1056
Asn	Arg	Tyr	Gln	Gln	Tyr	Gly	Ala	Glu	Glu	Cys	Val	Leu	Gln	Met	Gly		
				340					345						350		
ggt	gtg	ctg	tgc	ccc	cgt	cct	ggc	tgc	gga	gct	ggg	ctg	ctg	cct	gaa		1104
Gly	Val	Leu	Cys	Pro	Arg	Pro	Gly	Cys	Gly	Ala	Gly	Leu	Leu	Pro	Glu		
				355					360						365		

FRAV2002-0020 Sequence Listing.ST25.txt

cag ggc cag aag aaa gtc acc tgt gaa ggg ggc aac ggc ctg ggc tgt Gln Gly Gln Lys Lys Val Thr Cys Glu Gly Gly Asn Gly Leu Gly Cys 370 375 380	1152
ggg ttc gtt ttc tgc cg ^g gac tgc aag gaa gca tac cat gaa ggg gag Gly Phe Val Phe Cys Arg Asp Cys Lys Glu Ala Tyr His Glu Gly Glu 385 390 395 400	1200
tgc gac tcg atg ttc gaa gcc tcg ggg gcg act tct cag gca tac cgg Cys Asp Ser Met Phe Glu Ala Ser Gly Ala Thr Ser Gln Ala Tyr Arg 405 410 415	1248
gtg gat caa aga gct gct gag caa gca cg ^g tgg gag gag gcc tcc aag Val Asp Gln Arg Ala Ala Glu Gln Ala Arg Trp Glu Glu Ala Ser Lys 420 425 430	1296
gaa acc atc aag aaa acc acc aag cct tgt cct cgc tgc aat gtg ccc Glu Thr Ile Lys Lys Thr Thr Lys Pro Cys Pro Arg Cys Asn Val Pro 435 440 445	1344
att gaa aag aat gga gga tgt atg cac atg aag tgt cct cag ccc cag Ile Glu Lys Asn Gly Gly Cys Met His Met Lys Cys Pro Gln Pro Gln 450 455 460	1392
tgc aag ctg gag tgg tgt tgg aac tgc ggc tgt gag tgg aac cga gcc Cys Lys Leu Glu Trp Cys Trp Asn Cys Gly Cys Glu Trp Asn Arg Ala 465 470 475 480	1440
tgc atg ggt gat cac tgg ttt gac gtg tag Cys Met Gly Asp His Trp Phe Asp Val 485	1470

<210> 14
<211> 489
<212> PRT
<213> Rattus norvegicus

<400> 14

Met Ile Val Phe Val Arg Phe Asn Ser Ser Tyr Gly Phe Pro Val Glu
1 5 10 15

Val Asp Ser Asp Thr Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys
20 25 30

Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys
35 40 45

Glu Leu Gln Asn His Leu Thr Val Gln His Pro Gln Asp Gly Phe Cys
50 55 60

His Lys Ser His Leu Ala Val His Asn Leu Ser Gln Gln Asp Val Thr
65 70 75 80

Gln Asn Cys Asp Leu Glu Gln Gln Ser Ile Val His Ile Val Gln Arg
85 90 95

FRAV2002-0020 Sequence Listing.ST25.txt

Pro Gln Arg Lys Ser His Glu Thr Asn Ala Ser Gly Gly Asp Lys Pro
100 105 110

Gln Ser Thr Pro Glu Gly Ser Ile Trp Glu Pro Arg Ser Leu Thr Arg
115 120 125

Val Asp Leu Ser Ser His Ile Leu Pro Ala Asp Ser Val Gly Leu Ala
130 135 140

Val Ile Leu Asp Thr Asp Ser Lys Ser Asp Ser Glu Ala Ala Arg Gly
145 150 155 160

Pro Glu Ala Lys Pro Thr Tyr His Ser Phe Phe Val Tyr Cys Lys Gly
165 170 175

Pro Cys His Lys Val Gln Pro Gly Lys Leu Arg Val Gln Cys Gly Thr
180 185 190

Cys Arg Gln Ala Thr Leu Thr Leu Ala Gln Gly Pro Ser Cys Trp Asp
195 200 205

Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser Pro Asp
210 215 220

Cys Pro Gly Thr Arg Ala Glu Phe Phe Lys Cys Gly Ala His Pro
225 230 235 240

Thr Ser Asp Lys Asp Thr Ser Val Ala Leu Asn Leu Ile Thr Asn Asn
245 250 255

Ser Arg Ser Ile Pro Cys Ile Ala Cys Thr Asp Val Arg Asn Pro Val
260 265 270

Leu Val Phe Gln Cys Asn His Arg His Val Ile Cys Leu Asp Cys Phe
275 280 285

His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val His Asp
290 295 300

Ala Gln Leu Gly Tyr Ser Leu Pro Cys Val Ala Gly Cys Pro Asn Ser
305 310 315 320

Leu Ile Lys Glu Leu His His Phe Arg Ile Leu Gly Glu Glu Gln Tyr
325 330 335

Asn Arg Tyr Gln Gln Tyr Gly Ala Glu Glu Cys Val Leu Gln Met Gly
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FRAV2002-0020 Sequence Listing.ST25.txt
340 345 350

Gly Val Leu Cys Pro Arg Pro Gly Cys Gly Ala Gly Leu Leu Pro Glu
355 360 365

Gln Gly Gln Lys Lys Val Thr Cys Glu Gly Gly Asn Gly Leu Gly Cys
370 375 380

Gly Phe Val Phe Cys Arg Asp Cys Lys Glu Ala Tyr His Glu Gly Glu
385 390 395 400

Cys Asp Ser Met Phe Glu Ala Ser Gly Ala Thr Ser Gln Ala Tyr Arg
405 410 415

Val Asp Gln Arg Ala Ala Glu Gln Ala Arg Trp Glu Glu Ala Ser Lys
420 425 430

Glu Thr Ile Lys Lys Thr Thr Lys Pro Cys Pro Arg Cys Asn Val Pro
435 440 445

Ile Glu Lys Asn Gly Gly Cys Met His Met Lys Cys Pro Gln Pro Gln
450 455 460

Cys Lys Leu Glu Trp Cys Trp Asn Cys Gly Cys Glu Trp Asn Arg Ala
465 470 475 480

Cys Met Gly Asp His Trp Phe Asp Val
485

<210> 15
<211> 489
<212> PRT
<213> Rattus norvegicus

<400> 15

Met Ile Val Phe Val Arg Phe Asn Ser Ser Tyr Gly Phe Pro Val Glu
1 5 10 15

Val Asp Ser Asp Thr Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys
20 25 30

Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys
35 40 45

Glu Leu Gln Asn His Leu Thr Val Gln His Pro Gln Asp Gly Phe Cys
50 55 60

His Lys Ser His Leu Ala Val His Asn Leu Ser Gln Gln Asp Val Thr
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Gln Asn Cys Asp Leu Glu Gln Gln Ser Ile Val His Ile Val Gln Arg
 85 90 95

Pro Gln Arg Lys Ser His Glu Thr Asn Ala Ser Gly Gly Asp Lys Pro
 100 105 110

Gln Ser Thr Pro Glu Gly Ser Ile Trp Glu Pro Arg Ser Leu Thr Arg
 115 120 125

Val Asp Leu Ser Ser His Ile Leu Pro Ala Asp Ser Val Gly Leu Ala
 130 135 140

Val Ile Leu Asp Thr Asp Ser Lys Ser Asp Ser Glu Ala Ala Arg Gly
 145 150 155 160

Pro Glu Ala Lys Pro Thr Tyr His Ser Phe Phe Val Tyr Cys Lys Gly
 165 170 175

Pro Cys His Lys Val Gln Pro Gly Lys Leu Arg Val Gln Cys Gly Thr
 180 185 190

Cys Arg Gln Ala Thr Leu Thr Leu Ala Gln Gly Pro Ser Cys Trp Asp
 195 200 205

Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser Pro Asp
 210 215 220

Cys Pro Gly Thr Arg Ala Glu Phe Phe Phe Lys Cys Gly Ala His Pro
 225 230 235 240

Thr Ser Asp Lys Asp Thr Ser Val Ala Leu Asn Leu Ile Thr Asn Asn
 245 250 255

Ser Arg Ser Ile Pro Cys Ile Ala Cys Thr Asp Val Arg Asn Pro Val
 260 265 270

Leu Val Phe Gln Cys Asn His Arg His Val Ile Cys Leu Asp Cys Phe
 275 280 285

His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val His Asp
 290 295 300

Ala Gln Leu Gly Tyr Ser Leu Pro Cys Val Ala Gly Cys Pro Asn Ser
 305 310 315 320

FRAV2002-0020 Sequence Listing.ST25.txt

Leu Ile Lys Glu Leu His His Phe Arg Ile Leu Gly Glu Glu Gln Tyr
325 330 335

Asn Arg Tyr Gln Gln Tyr Gly Ala Glu Glu Cys Val Leu Gln Met Gly
340 345 350

Gly Val Leu Cys Pro Arg Pro Gly Cys Gly Ala Gly Leu Leu Pro Glu
355 360 365

Gln Gly Gln Lys Lys Val Thr Cys Glu Gly Gly Asn Gly Leu Gly Cys
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Gly Phe Val Phe Cys Arg Asp Cys Lys Glu Ala Tyr His Glu Gly Glu
385 390 395 400

Cys Asp Ser Met Phe Glu Ala Ser Gly Ala Thr Ser Gln Ala Tyr Arg
405 410 415

Val Asp Gln Arg Ala Ala Glu Gln Ala Arg Trp Glu Glu Ala Ser Lys
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Glu Thr Ile Lys Lys Thr Thr Lys Pro Cys Pro Arg Cys Asn Val Pro
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Ile Glu Lys Asn Gly Gly Cys Met His Met Lys Cys Pro Gln Pro Gln
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Cys Lys Leu Glu Trp Cys Trp Asn Cys Gly Cys Glu Trp Asn Arg Ala
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Cys Met Gly Asp His Trp Phe Asp Val
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